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=> d his

     (FILE 'HOME' ENTERED AT 21:53:40 ON 25 NOV 2008)

     FILE 'MEDLINE, CAPLUS, BIOSIS, SCISEARCH, LIFESCI' ENTERED AT 21:54:08 ON
     25 NOV 2008
L1          4584 S RNA(6A)(DIFFERENT? OR DEVIAT? OR DISCRE?)(6A)(POLYPEPTIDE OR
L2         53739 S EMBRYONIC(W)STEM(W)CELL OR ES(W)CELL
L3         69946 S SOMATIC(W)CELL
L4         11201 S ADULT(3A)STEM(W)CELL
L5            14 S L1(P)L2
L6         80894 S L3 OR L4
L7             0 S L5 AND L6
L8             1 S L1 AND L2 AND L6
L9            10 DUP REM L5 (4 DUPLICATES REMOVED)

=> d au ti so pi ab 1-10 l9

L9   ANSWER 1 OF 10  LIFESCI    COPYRIGHT 2008 CSA on STN
AU   Masaki, Hisaharu; Nishida, Tomohiro; Kitajima, Shigetaka; Asahina, Kinji;
     Teraoka, Hirobumi
TI   Developmental Pluripotency-associated 4 (DPPA4) Localized in Active
     Chromatin Inhibits Mouse Embryonic Stem Cell Differentiation into a
     Primitive Ectoderm Lineage
SO   Journal of Biological Chemistry [J. Biol. Chem.], (20071109) vol. 282, no.
     45, pp. 33034-33042.
     ISSN: 0021-9258.
AB   Because embryonic stem (ES) cells can proliferate
     indefinitely in an undifferentiated state and differentiate into various
     cell types, ES cells are expected to be useful for
     cell replacement therapy and basic research on early embryogenesis.
     Although molecular mechanisms of ES cell self-renewal
     have been studied, many uncharacterized genes expressed in ES
     cells remain to be clarified. Developmental pluripotency
     associated 4 (Dppa4) is one such gene highly expressed in both ES
     cells and early embryos. Here, we investigated the role of Dppa4
     in mouse ES cell self-renewal and differentiation. We
     generated Dppa4-overexpressing ES cells under the
     control of tetracycline. Dppa4 overexpression suppressed cell
     proliferation and formation of embryoid bodies and caused massive cell
     death in differentiating ES cells. Quantitative
     reverse transcription-PCR analysis showed that Dppa4 overexpression does
     not support ES cell self-renewal but partially
     inhibits ES cell differentiation. Suppression of Dppa4
     expression by short hairpin RNA induced ES
     cell differentiation into a primitive ectoderm lineage.
     DPPA4 protein was localized in the ES cell
     nucleus associated with chromatin. Micrococcal nuclease digestion analysis
     and immunocytochemistry revealed that DPPA4 is associated with
     transcriptionally active chromatin. These findings indicate that DPPA4 is
     a nuclear factor associated with active chromatin and that it regulates
     differentiation of ES cells into a primitive ectoderm
     lineage.

L9   ANSWER 2 OF 10     MEDLINE on STN                  DUPLICATE 1
AU   Hirst Martin; Delaney Allen; Rogers Sean A; Schnerch Angelique; Persaud
     Deryck R; O'Connor Michael D; Zeng Thomas; Moksa Michelle; Fichter Keith;
     Mah Diana; Go Anne; Morin Ryan D; Baross Agnes; Zhao Yongjun; Khattra
     Jaswinder; Prabhu Anna-Liisa; Pandoh Pawan; McDonald Helen; Asano
     Jennifer; Dhalla Noreen; Ma Kevin; Lee Stephanie; Ally Adrian; Chahal
     Neil; Menzies Stephanie; Siddiqui Asim; Holt Robert; Jones Steven; Gerhard
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Daniela S; Thomson James A; Eaves Connie J; Marra Marco A
TI LongSAGE profiling of nine human embryonic stem cell lines.
SO Genome biology, (2007) Vol. 8, No. 6, pp. R113.
Journal code: 100960660. E-ISSN: 1465-6914.
AB To facilitate discovery of novel human embryonic stem
cell (ESC) transcripts, we generated 2.5 million LongSAGE tags
from 9 human ESC lines. Analysis of this data revealed that ESCs express
proportionately more RNA binding proteins compared
with terminally differentiated cells, and identified novel ESC
transcripts, at least one of which may represent a marker of the
pluripotent state.

L9 ANSWER 3 OF 10 CAPLUS COPYRIGHT 2008 ACS on STN
AU Hirst, Martin; Delaney, Allen; Rogers, Sean A.; Schnerch, Angelique;
Persaud, Deryck R.; O'Connor, Michael D.; Zeng, Thomas; Moksa, Michelle;
Fichter, Keith; Mah, Diana; Go, Anne; Morin, Ryan D.; Baross, Agnes; Zhao,
Yongjun; Khattra, Jaswinder; Prabhu, Anna-Liisa; Pandoh, Pawan; McDonald,
Helen; Asano, Jennifer; Dhalla, Noreen; Ma, Kevin; Lee, Stephanie; Ally,
Adrian; Chahal, Neil; Menzies, Stephanie; Siddiqui, Asim; Holt, Robert;
Jones, Steven; Gerhard, Daniela S.; Thomson, James A.; Eaves, Connie J.;
Marra, Marco A.
TI LongSAGE profiling of nine human embryonic stem cell lines
SO GenomeBiology (2007), 8(6), No pp. given
CODEN: GNBLFW; ISSN: 1465-6914
URL: http://genomebiology.com/content/pdf/gb-2007-8-6-r113.pdf
AB To facilitate discovery of novel human embryonic stem
cell (ESC) transcripts, the authors generated 2.5 million LongSAGE
tags from 9 human ESC lines. Anal. of this data revealed that ESCs
express proportionately more RNA binding proteins
compared with terminally differentiated cells, and identified
novel ESC transcripts, at least one of which may represent a marker of the
pluripotent state.

L9 ANSWER 4 OF 10 MEDLINE on STN
AU Aghajanova Lusine; Skottman Heli; Stromberg Anne-Marie; Inzunza Jose;
Lahesmaa Riitta; Hovatta Outi
TI Expression of leukemia inhibitory factor and its receptors is increased
during differentiation of human embryonic stem cells.
SO Fertility and sterility, (2006 Oct) Vol. 86, No. 4 Suppl, pp. 1193-209.
Electronic Publication: 2006-09-01.
Journal code: 0372772. E-ISSN: 1556-5653.
AB OBJECTIVE: To investigate gene expression profiles during the early
spontaneous differentiation of human embryonic stem
cells (hESCs), with particular emphasis on leukemia inhibitory
factor (LIF)-induced pathways and the ultrastructural surface morphology
of the undifferentiated and spontaneously differentiated hESCs. DESIGN:
Prospective experimental study. SETTING: University laboratory.
PATIENT(S): Four hESC cell lines. INTERVENTION(S): The effect of LIF on
receptor expression level was studied in cultures. MAIN OUTCOME
MEASURE(S): Gene expression in the hESC line HS237 was analyzed using
microarrays. Real-time reverse-transcription polymerase chain reaction
was used to validate the microarray results in four hESC lines (HS181,
HS235, HS237, HS293). Immunohistochemistry was used to assay LIF, LIF
receptor, and gp130 protein expression. Cell surface morphology was
studied using scanning electron microscopy. RESULT(S): The expression of
LIF, LIF receptor, and gp130 messenger RNA and protein
was increased in spontaneously differentiated HS237 cells
compared with undifferentiated cells, with high expression of an inhibitor
of LIF-mediated signaling, suppressor of cytokine signaling-1, in
undifferentiated hESCs. Genes, those expressed specifically and those
shared in undifferentiated hESCs, differentiated cells, and in

fibroblasts, were identified. Supplementation with LIF did not affect the LIF receptor expression. CONCLUSION(S): The expression of LIF and its receptors is low in undifferentiated hESCs but increases during differentiation. Added LIF does not prevent spontaneous differentiation. Suppressor of cytokine signaling-1 may prevent LIF signaling in hESCs.

L9 ANSWER 5 OF 10 BIOSIS COPYRIGHT (c) 2008 The Thomson Corporation on STN
AU Aghajanova, Lusine [Reprint Author]; Skottman, Heli; Stromberg, Anne-Marie; Inzunza, Jose; Lahesmaa, Riitta; Hovatta, Outi
TI Expression of leukemia inhibitory factor and its receptors is increased during differentiation of human embryonic stem cells.
SO Fertility and Sterility, (OCT 2006) Vol. 86, No. Suppl. 3, pp. 1193-1209. CODEN: FESTAS. ISSN: 0015-0282.
AB Objective: To investigate gene expression profiles during the early spontaneous differentiation of human embryonic stem cells (hESCs), with particular emphasis on leukemia inhibitory factor (LIF)-induced pathways and the ultrastructural surface morphology of the undifferentiated and spontaneously differentiated hESCs.Design: Prospective experimental study.Setting: University laboratory.Patient(s): Four hESC cell lines.Intervention(s): The effect of LIF on receptor expression level was studied in cultures.Main Outcome Measure(s): Gene expression in the hESC line HS237 was analyzed using microarrays. Real-time reverse-transcription polymerase chain reaction was used to validate the microarray results in four hESC lines (HS181, HS235, hs237, HS293). Immunohistochemistry was used to assay LIF, LIF receptor, and gp130 protein expression. Cell surface morphology was studied using scanning electron microscopy.Result(s): The expression of LIF, LIF receptor, and gp130 messenger RNA and protein was increased in spontaneously differentiated HS237 cells compared with undifferentiated cells, with high expression of an inhibitor of LIF-mediated signaling, suppressor of cytokine signaling-1, in undifferentiated hESCs. Genes, those expressed specifically and those shared in undifferentiated hESCs, differentiated cells, and in fibroblasts, were identified. Supplementation with LIF did not affect the LIF receptor expression.Conclusion(s): The expression of LIF and its receptors is low in undifferentiated hESCs but increases during differentiation. Added LIF does not prevent spontaneous differentiation. Suppressor of cytokine signaling-1 may prevent LIF signaling in hESCs.

L9 ANSWER 6 OF 10 CAPLUS COPYRIGHT 2008 ACS on STN
IN Andrews, Peter; Walsh, James; Gokhale, Paul
TI Method for modulating stem cell differentiation using stem loop RNA
SO PCT Int. Appl., 85 pp.
CODEN: PIXXD2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2003012082	A2	20030213	WO 2002-GB3409	20020725
WO 2003012082	A3	20040610		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

AU 2002355785 A1 20030217 AU 2002-355785 20020725

AB This invention relates to a method to promote the differentiation of stem cells, typically embryonic stem cells,

through the use of RNA interference, by the introduction of stem loop RNA into a cell. Further, the invention relates to a method to modulate stem cell differentiation comprising introducing stem loop containing RNA into a stem cell to ablate mRNA's which encode polypeptides which are involved in stem cell differentiation; stem loop RNA 's; and nucleic acid mols. and vectors encoding stem loop RNA's.

L9 ANSWER 7 OF 10 CAPLUS COPYRIGHT 2008 ACS on STN
AU Bain, G.; Mansergh, F. C.; Wride, M. A.; Hance, J. E.; Isogawa, A.; Rancourt, S. L.; Ray, W. J.; Yoshimura, Y.; Tsuzuki, T.; Gottlieb, D. I.; Rancourt, D. E.
TI ES cell neural differentiation reveals a substantial number of novel ESTs. [Erratum to document cited in CA135:150370]
SO Functional & Integrative Genomics (2000), 1(3), 218-219
CODEN: FIGUBY; ISSN: 1438-793X
AB The captions for Figure 1 and Figure 2 were reversed.

L9 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2008 ACS on STN
AU Bain, G.; Mansergh, F. C.; Wride, M. A.; Hance, J. E.; Isogawa, A.; Rancourt, S. L.; Ray, W. J.; Yoshimura, Y.; Tsuzuki, T.; Gottlieb, D. I.; Rancourt, D. E.
TI ES cell neural differentiation reveals a substantial number of novel ESTs
SO Functional & Integrative Genomics (2000), 1(2), 127-139
CODEN: FIGUBY; ISSN: 1438-793X
AB A method was used for synchronously differentiating murine embryonic stem (ES) cells into functional neurons and glia in culture. Using subtractive hybridization, .apprx.1200 cDNA clones were isolated from ES cell cultures at the neural precursor stage of neural differentiation. Pilot studies indicated that this library is a good source of novel neuro-embryonic cDNA clones. Therefore, the entire library was screened by single-pass sequencing. Characterization of 604 non-redundant cDNA clones by BLAST revealed 96 novel expressed sequence tags (ESTs) and an addnl. 197 matching uncharacterized ESTs or genomic clones derived from genome sequencing projects. With the exception of a handful of genes, whose functions are still unclear, most of the 311 known genes identified in this screen are expressed in embryonic development and/or the nervous system. At least 80 of these genes are implicated in disorders of differentiation, neural development, and/or neural function. This study provides an initial snapshot of gene expression during early neural differentiation of ES cell cultures. Given the recent identification of human ES cells, further characterization of these novel and uncharacterized ESTs has the potential to identify genes that may be important in nervous system development, physiol., and disease.

L9 ANSWER 9 OF 10 MEDLINE on STN DUPLICATE 2
AU Su W; Shmukler B E; Chernova M N; Stuart-Tilley A K; de Franceschi L; Brugnara C; Alper S L
TI Mouse K-Cl cotransporter KCC1: cloning, mapping, pathological expression, and functional regulation.
SO The American journal of physiology, (1999 Nov) Vol. 277, No. 5 Pt 1, pp. C899-912.
Journal code: 0370511. ISSN: 0002-9513.
AB Although K-Cl cotransporter (KCC1) mRNA is expressed in many tissues, K-Cl cotransport activity has been measured in few cell types, and detection of endogenous KCC1 polypeptide has not yet been reported. We have cloned the mouse erythroid KCC1 (mKCC1) cDNA and its flanking genomic regions and mapped the mKCC1 gene to chromosome 8. Three anti-peptide antibodies raised against recombinant mKCC1 function as immunoblot and immunoprecipitation reagents. The tissue distributions of mKCC1 mRNA and protein are widespread, and mKCC1 RNA is constitutively expressed during erythroid differentiation of ES

cells. KCC1 polypeptide or related antigen is present in erythrocytes of multiple species in which K-Cl cotransport activity has been documented. Erythroid KCC1 polypeptide abundance is elevated in proportion to reticulocyte counts in density-fractionated cells, in bleeding-induced reticulocytosis, in mouse models of sickle cell disease and thalassemia, and in the corresponding human disorders. mKCC1-mediated uptake of (86)Rb into Xenopus oocytes requires extracellular Cl(-), is blocked by the diuretic R(+)-[2-n-butyl-6,7-dichloro-2-cyclopentyl-2,3-dihydro-1-oxo-1H-indenyl-5-yl-)oxy]acetic acid, and exhibits an erythroid pattern of acute regulation, with activation by hypotonic swelling, N-ethylmaleimide, and staurosporine and inhibition by calyculin and okadaic acid. These reagents and findings will expedite studies of KCC1 structure-function relationships and of the pathobiology of KCC1-mediated K-Cl cotransport.

L9 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2008 ACS on STN
AU Oyamada, Yumiko; Komatsu, Kiyoshi; Kimura, Hisakazu; Mori, Michio; Oyamada, Masahito
TI Differential regulation of gap junction protein (connexin) genes during cardiomyocytic differentiation of mouse embryonic stem cells in vitro
SO Experimental Cell Research (1996), 229(2), 318-326
CODEN: ECREAL; ISSN: 0014-4827
AB Using an in vitro system for differentiation of embryonic stem (ES) cells into cardiac myocytes, we analyzed the expression of connexin (Cx) genes by RT-PCR to learn what changes in the expression of multiple connexin genes occur during the early stage of heart development. We also examined gap junctional intercellular communication by using Lucifer Yellow dye microinjection transfer, studied intracellular Ca2+ transients by confocal laser image anal. using fluo 3, and determined localization of Cx43 by immunofluorescence during in vitro differentiation of ES cells into cardiac myocytes. The transcripts for Cx43 and Cx45 were detected in undifferentiated ES cells and in embryoid bodies before and after the appearance of beating cardiomyocytes. In contrast, Cx40 transcripts were not observed in undifferentiated ES cells and were barely detectable in 3- and 5-day-old embryoid bodies. Cx40 transcripts significantly increased with the appearance of beating cells similar to those of cardiac-specific genes. Dye coupling was present among undifferentiated ES cells, prebeating cells of embryoid body outgrowth and ES cell-derived beating cardiomyocytes. When dye was injected into a beating cell, dye spread was restricted to neighboring beating cells. Immunofluorescence demonstrated that Cx43 protein was localized not only in beating cells but also in surrounding nonbeating cells, whereas myosin heavy chain α/β was exclusively pos. in the beating cells. These data suggest that the expression of multiple connexins is differentially regulated during the cardiomyocytic differentiation of ES cells in vitro and that Cx40 expression may be linked to early stages in cardiomyocytic differentiation.

=> d bib ab 18

L8 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2007:618222 CAPLUS
DN 147:46109
TI The differentiation-associated zinc finger protein SALL4 in the diagnosis and treatment of proliferative disorders associated with myelodysplastic syndrome
IN Ma, Yupo
PA Nevada Cancer Institute, USA
SO PCT Int. Appl., 163pp.
CODEN: PIXXD2

DT Patent
LA English
FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2007064696	A2	20070607	WO 2006-US45672	20061129
	WO 2007064696	A3	20080703		
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW			
	RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AP, EA, EP, OA			
	AU 2006320654	A1	20070607	AU 2006-320654	20061129
	CA 2631312	A1	20070607	CA 2006-2631312	20061129
	EP 1959728	A2	20080827	EP 2006-844627	20061129
	R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LI, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, AL, BA, HR, MK, RS				
PRAI	US 2005-741015P	P	20051129		
	WO 2006-US45672	W	20061129		

AB New members of the spalt family of zinc finger proteins, SALL4 and the splicing isoforms SALL4A, SALL4B, and SALL4C, are identified as playing a role in myelopoiesis and in myelodysplastic syndrome. The genes and proteins may therefore be useful in the diagnosis and therapy of myelodysplastic syndrome and related proliferative disorders. Constitutive expression of SALL4 increases leukemogenic potential in cells of model animal systems. Constitutive expression of select isoforms (e.g., SALL4B) in transgenic mice demonstrate that these animals develop myelodysplastic syndrome-like signs and symptoms, including subsequent acute myeloid leukemia (AML), which is transplantable. The disclosure also provides methods for identifying and purifying embryonic stem cells, adult stem cells , cancer stem cells, including leukemia stem cells, methods for identifying substances which bind to and/or modulate SALL4, methods for diagnosing MDS in a subject, and methods of treating a subject presenting MDS.

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